

- 1 -

SEQUENCE LISTING

<110> DANA-FARBER CANCER INSTITUTE

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<150> USSN 60/106,383

<151> 1998-10-29

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<170> PatentIn Ver. 2.0

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Thr Ser Leu Ser Leu Leu Phe Gln Lys Val Phe Ala Gln Ile Phe Pro
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Lys	Leu	Gln	Arg	Ala	Ile	Val	Ser	Ile	Leu	Asn	Tyr	Val	Ile	Tyr	Lys	
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Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser Ser Glu Met

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2890

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Cys Thr Gly Lys Leu Gln Arg Ala Ile Val Ser Ile Leu Asn Tyr Val 210 215 220		
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Ser Gly Ile Phe Gln Phe Pro Leu Asn Leu Cys Thr Lys Thr Ile Val 245 250 255		
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Thr Thr Pro Ser Phe Asn Ala Met Val Val Asn Asn Leu Thr Leu Gln 305 310 315 320		
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Ser Val Asn Pro His Asp Ile Thr Val Gly Pro Val Ala Lys Ser Ile 340 345 350		
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Cys Ile Glu Gln Asn Ile Thr Ser Ile Ser Phe Pro Ala Leu Gly Thr 420 425 430		
Gly Asn Met Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp 435 440 445		

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Thr	Thr	Pro	Ser	Phe	Asn	Ala	Met	Val	Val	Asn	Asn	Leu	Thr	Leu	Gln															
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1008																														
Ile	Val	Gln	Gly	His	Ile	Glu	Trp	Gln	Thr	Ala	Asp	Val	Ile	Val	Asn															
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- 11 -

tct gta aac cca cat gat att aca gtt gga cct gtg gca aag tca att
1056

Ser Val Asn Pro His Asp Ile Thr Val Gly Pro Val Ala Lys Ser Ile
340 345 350

cta caa caa gca gga gtt gaa atg aaa tcg gaa ttt ctt gcc aca aag
1104

Leu Gln Gln Ala Gly Val Glu Met Lys Ser Glu Phe Leu Ala Thr Lys
355 360 365

gct aaa cag ttt caa cgg tcc cag ttg gta ctg gtc aca aaa gga ttt
1152

Ala Lys Gln Phe Gln Arg Ser Gln Leu Val Leu Val Thr Lys Gly Phe
370 375 380

aac ttg ttc tgt aaa tat ata tac cat gta ctg tgg cat tca gaa ttt
1200

Asn Leu Phe Cys Lys Tyr Ile Tyr His Val Leu Trp His Ser Glu Phe
385 390 395 400

cct aaa cct cag ata tta aaa cat gca atg aag gag tgt ttg gaa aaa
1248

Pro Lys Pro Gln Ile Leu Lys His Ala Met Lys Glu Cys Leu Glu Lys
405 410 415

tgc att gag caa aat ata act tcc att tcc ttt cct gcc ctt ggg act
1296

Cys Ile Glu Gln Asn Ile Thr Ser Ile Ser Phe Pro Ala Leu Gly Thr
420 425 430

gga aac atg gaa ata aag aag gaa aca gca gca gag att ttg ttt gat
1344

Gly Asn Met Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp
435 440 445

gaa gtt tta aca ttt gcc aaa gac cat gta aaa cac cag tta act gta
1392

Glu Val Leu Thr Phe Ala Lys Asp His Val Lys His Gln Leu Thr Val
450 455 460

aaa ttt gtg atc ttt cca aca gat ttg gag ata tat aag gct ttc agt
1440

Lys Phe Val Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser
465 470 475 480

tct gaa atg gca aag agg tcc aag atg ctg agt ttg aac aat tac agt
1488

Ser Glu Met Ala Lys Arg Ser Lys Met Leu Ser Leu Asn Asn Tyr Ser
485 490 495

gtc ccc cag tca acc aga gag gag aaa aga gaa aat ggg ctt gaa gct
1536

Val Pro Gln Ser Thr Arg Glu Glu Lys Arg Glu Asn Gly Leu Glu Ala
500 505 510

aga tct cct gcc atc aat ctg atg gga ttc aac gtg gaa gag atg tat

- 12 -

1584

Arg Ser Pro Ala Ile Asn Leu Met Gly Phe Asn Val Glu Glu Met Tyr
 515 520 525

gag gcc cac gca tgg atc caa aga atc ctg agt ctc cag aac cac cac
 1632

Glu Ala His Ala Trp Ile Gln Arg Ile Leu Ser Leu Gln Asn His His
 530 535 540

atc att gag aat aat cat att ctg tac ctt ggg aga aag gaa cat gac
 1680

Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Arg Lys Glu His Asp
 545 550 555 560

att ttg tct cag ctt cag aaa act tca agt gtc tcc atc aca gaa att
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Ile Leu Ser Gln Leu Gln Lys Thr Ser Ser Val Ser Ile Thr Glu Ile
 565 570 575

atc agc cca gga agg aca gag tta gag att gaa gga gcc cgg gct gac
 1776

Ile Ser Pro Gly Arg Thr Glu Leu Glu Ile Glu Gly Ala Arg Ala Asp
 580 585 590

ctc att gag gtg gtt atg aac att gaa gat atg ctt tgt aaa gta cag
 1824

Leu Ile Glu Val Val Met Asn Ile Glu Asp Met Leu Cys Lys Val Gln
 595 600 605

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 1872

Glu Glu Met Ala Arg Lys Lys Glu Arg Gly Leu Trp Arg Ser Leu Gly
 610 615 620

cag tgg act att cag caa caa aaa acc caa gac gaa atg aaa gaa aat
 1920

Gln Trp Thr Ile Gln Gln Gln Lys Thr Gln Asp Glu Met Lys Glu Asn
 625 630 635 640

atc ata ttt ctg aaa tgt cct gtg cct cca act caa gag ctt cta gat
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caa aag aaa cag ttt gaa aaa tgt ggt ttg cag gtt cta aag gtg gag
 2016

Gln Lys Lys Gln Phe Glu Lys Cys Gly Leu Gln Val Leu Lys Val Glu
 660 665 670

aag ata gac aat gag gtc ctt atg gct gcc ttt caa aga aag aag aaa
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Lys Ile Asp Asn Glu Val Leu Met Ala Ala Phe Gln Arg Lys Lys Lys
 675 680 685

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 2112

Met Met Glu Glu Lys Leu His Arg Gln Pro Val Ser His Arg Leu Phe
 690 695 700

1584
1632
1680
1728
1776
1824
1872
1920
1968
2016
2064
2112

- 13 -

cag caa gtc cca tac cag ttc tgc aat gtg gta tgc aga gtt ggc ttt
2160

Gln Gln Val Pro Tyr Gln Phe Cys Asn Val Val Cys Arg Val Gly Phe
705 710 715 720

caa aga atg tac tcg aca cct tgc gat cca aaa tac gga gct ggc ata
2208

Gln Arg Met Tyr Ser Thr Pro Cys Asp Pro Lys Tyr Gly Ala Gly Ile
725 730 735

tac ttc acc aag aac ctc aaa aac ctg gca gag aag gcc aag aaa atc
2256

Tyr Phe Thr Lys Asn Leu Lys Asn Leu Ala Glu Lys Ala Lys Lys Ile
740 745 750

tct gct gca gat aag ctg atc tat gtg ttt gag gct gaa gta ctc acà
2304

Ser Ala Ala Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr
755 760 765

ggc ttc ttc tgc cag gga cat ccg tta aat att gtt ccc cca cca ctg
2352

Gly Phe Phe Cys Gln Gly His Pro Leu Asn Ile Val Pro Pro Pro Leu
770 775 780

agt cct gga gct ata gat ggt cat gac agt gtg gtt gac aat gtc tcc
2400

Ser Pro Gly Ala Ile Asp Gly His Asp Ser Val Val Asp Asn Val Ser
785 790 795 800

agc cct gaa acc ttt gtt att ttt agt ggc atg cag gct ata cct cag
2448

Ser Pro Glu Thr Phe Val Ile Phe Ser Gly Met Gln Ala Ile Pro Gln
805 810 815

tat ttg tgg aca tgc acc cag gaa tat gta cag tca caa gat tac tca
2496

Tyr Leu Trp Thr Cys Thr Gln Glu Tyr Val Gln Ser Gln Asp Tyr Ser
820 825 830

tca gga cca atg aga ccc ttt gca cag cat cct tgg agg gga ttc gca
2544

Ser Gly Pro Met Arg Pro Phe Ala Gln His Pro Trp Arg Gly Phe Ala
835 840 845

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2562

Ser Gly Ser Pro Val Asp
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<211> 3024

<212> DNA

<213> Murinae gen. sp.

<220>

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<222> (171)..(2648)

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aaatataaat atctgaagac ccacgtggga cctgaagaat ggccctattac atg gat      176
                                         Met Asp
                                         1

aca tgg gcg gca gct ccc gcc gaa aga cca gcc aac aat tct ctt gaa 224
Thr Trp Ala Ala Ala Pro Ala Glu Arg Pro Ala Asn Asn Ser Leu Glu
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gaa cat tat aga tgg caa att ccc att aaa cac aat gtc ttc gaa att 272
Glu His Tyr Arg Trp Gln Ile Pro Ile Lys His Asn Val Phe Glu Ile
                    20                      25                      30

tta aag agc aat gag agt cag cta tgt gaa gtc ctc caa aat aag ttt 320
Leu Lys Ser Asn Glu Ser Gln Leu Cys Glu Val Leu Gln Asn Lys Phe
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gga tgc atc tct acc ctg agc tgt cca act cta gca ggg agc agc tct 368
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cct gct cag aga gtc ttc aga agg acc ctg atc cct ggg ata gag tta 416
Pro Ala Gln Arg Val Phe Arg Arg Thr Leu Ile Pro Gly Ile Glu Leu
                    70                      75                      80

tct gtc tgg aag gat gac ctt acc aga cac gtt gtt gat gct gtg gtg 464
Ser Val Trp Lys Asp Asp Leu Thr Arg His Val Val Asp Ala Val Val
                    85                      90                      95

aac gca gcc aat gaa aac ctt ttg cat gga agt ggc ctg gcc gga agc 512
Asn Ala Ala Asn Glu Asn Leu Leu His Gly Ser Gly Leu Ala Gly Ser
                    100                      105                      110

ttg gtg aaa act ggt ggc ttt gaa atc caa gaa gag agc aaa aga atc 560
Leu Val Lys Thr Gly Gly Phe Glu Ile Gln Glu Glu Ser Lys Arg Ile
                    115                      120                      125                      130

att gcc aac gtt ggt aaa atc tca gtt ggt gga atc gct atc acc ggt 608
Ile Ala Asn Val Gly Lys Ile Ser Val Gly Gly Ile Ala Ile Thr Gly
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gcg ggg aga ctt cct tgc cat ttg att atc cat gcg gtt gga cct cgg 656
Ala Gly Arg Leu Pro Cys His Leu Ile Ile His Ala Val Gly Pro Arg
                    150                      155                      160

tgg aca gtt acg aac agc cag aca gct atc gaa tta ctg aaa ttt gcc 704
Trp Thr Val Thr Asn Ser Gln Thr Ala Ile Glu Leu Leu Lys Phe Ala
                    165                      170                      175

att agg aac att cta gat tat gtc acc aaa tat gat cta cgc att aag 752
Ile Arg Asn Ile Leu Asp Tyr Val Thr Lys Tyr Asp Leu Arg Ile Lys

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180	185	190	
aca gta gca att cca gcc ctg agc tct gga att ttc cag ttc cct ctg			800
Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile Phe Gln Phe Pro Leu			
195	200	205	210
gat ttg tgt aca agc ata att tta gaa act atc cgg ctt tat ttc caa			848
Asp Leu Cys Thr Ser Ile Ile Leu Glu Thr Ile Arg Leu Tyr Phe Gln			
	215	220	225
gac aag caa atg ttc ggt aat ttg aga gag att cat ctg gtg agc aat			896
Asp Lys Gln Met Phe Gly Asn Leu Arg Glu Ile His Leu Val Ser Asn			
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gag gac ccc act gtt gcg tcc ttt aaa tcc gcc tca gaa agc atc cta			944
Glu Asp Pro Thr Val Ala Ser Phe Lys Ser Ala Ser Glu Ser Ile Leu			
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ggg agg gac ctg agc tct tgg ggg ggt cca gaa act gac cct gct tcc			992
Gly Arg Asp Leu Ser Ser Trp Gly Gly Pro Glu Thr Asp Pro Ala Ser			
	260	265	270
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1040			
Thr Met Thr Leu Arg Ile Gly Arg Gly Leu Thr Leu Gln Ile Val Gln			
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ggc tgt att gaa atg caa aca aca gat gta att ggt aat tct gga tac			
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Gly Cys Ile Glu Met Gln Thr Thr Asp Val Ile Gly Asn Ser Gly Tyr			
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Ala Gly Val Glu Met Glu Lys Glu Leu Asp Lys Val Asn Leu Ser Thr			
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gat tat caa gag gtg tgg gtc aca aaa gga ttt aaa ttg tcc tgt cag			
1232			
Asp Tyr Gln Glu Val Trp Val Thr Lys Gly Phe Lys Leu Ser Cys Gln			
	340	345	350
tat gtc ttc cat gtg gca tgg cat tcc caa atc aac aaa tac cag ata			
1280			
Tyr Val Phe His Val Ala Trp His Ser Gln Ile Asn Lys Tyr Gln Ile			
355	360	365	370
ttg aaa gat gca atg aag tcc tgt cta gaa aaa tgc ctt aaa cca gat			
1328			
Leu Lys Asp Ala Met Lys Ser Cys Leu Glu Lys Cys Leu Lys Pro Asp			
	375	380	385
ata aat tcc att tcc ttt cct gct ctc ggg aca gga ttg atg gat ttg			

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1376

Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met Asp Leu
 390 395 400

aag aag agt aca gca gct cag ata atg ttt gag gaa gtt ttt gca ttt
 1424

Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe Ala Phe
 405 410 415

gct aaa gag cac aag gaa aaa acg cta act gta aag att gtg atc ttt
 1472

Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val Ile Phe
 420 425 430

cca gta gat gtg gag acg tac aag att ttt tat gct gaa atg aca aaa
 1520

Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met Thr Lys
 435 440 445 450

agg tcc aac gag ctg aat ctc agc ggt aat agt ggt gct tta gcc ctg
 1568

Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu Ala Leu
 455 460 465

cag tgg tcc agt ggg gag caa aga aga ggc ggc ctt gaa gct gga tct
 1616

Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala Gly Ser
 470 475 480

cct gcc atc aat ctc atg ggt gta aaa gtg gga gag atg tgt gag gcc
 1664

Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys Glu Ala
 485 490 495

cag gaa tgg att gaa agg ttg ctg gtc tcc ctg gac cac cac atc att
 1712

Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His Ile Ile
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gag aat aat cat att ctc tat ctt ggg aaa aaa gag cac gac gtg ctg
 1760

Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp Val Leu
 515 520 525 530

tct gag ctc cag acc agc aca aga gtc tcc att tca gag act gtc agt
 1808

Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr Val Ser
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cca aga acg gcc act ttg gag att aaa ggt ccc cag gct gac ctc att
 1856

Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp Leu Ile
 550 555 560

gac gca gtt atg agg att gaa tgt atg ctg tgt gac gtt cag gaa gaa
 1904

Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln Glu Glu
 565 570 575

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gtg gca gga aaa agg gag aaa aat ctt tgg agc ttg tca gga cag ggg
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Val Ala Gly Lys Arg Glu Lys Asn Leu Trp Ser Leu Ser Gly Gln Gly
580 585 590

acc aac cag caa gaa aaa ctg gat aaa atg gaa gaa tcg tac aca ttt
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Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr Thr Phe
595 600 605 610

caa cga tac cca gca tca tta act cag gaa ctt cag gac cga aag aaa
2048

Gln Arg Tyr Pro Ala Ser Leu Thr Gln Glu Leu Gln Asp Arg Lys Lys
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Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln Ile Asp
630 635 640

aat aag gtg ctg ctg gct gcc ttc caa gag aag aag aaa atg atg gaa
2144

Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met Met Glu
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2192

Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln Gln Val
660 665 670

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2240

Pro His Gln Phe Cys Asn Thr Val Cys Arg Val Gly Phe His Arg Met
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2288

Tyr Ser Thr Ser Tyr Asn Pro Val Tyr Gly Ala Gly Ile Tyr Phe Thr
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2336

Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser Ser Thr
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gac aag cta atc tat gtg ttt gag gca gaa gta ctc aca ggg tcc ttc
2384

Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly Ser Phe
725 730 735

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2432

Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser Pro Gly
740 745 750

gcc tta gat gtc aat gac agc gta gtt gac aat gtt tcc agc cct gaa
2480

- 18 -

Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser Pro Glu
755 760 765 770

acc att gtt gtt ttt aat ggc atg cag gcc atg ccc ctg tac ttg tgg
2528

Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr Leu Trp
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act tgc aca cag gat agg aca ttc tca cag cat ccg atg tgg tca cag
2576

Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp Ser Gln
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gac tac tca tca gga cca gga atg gtc tct tcg ctg cag tcc tgg gaa
2624

Asp Tyr Ser Ser Gly Pro Gly Met Val Ser Ser Leu Gln Ser Trp Glu
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2678

Trp Val Leu Asn Gly Ser Ser Val
820 825

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<213> Murinae gen. sp.

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Lys Phe Gly Cys Ile Ser Thr Leu Ser Cys Pro Thr Leu Ala Gly Ser

- 19 -

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Glu	Leu	Ser	Val	Trp	Lys	Asp	Asp	Leu	Thr	Arg	His	Val	Val	Asp	Ala	
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Val	Val	Asn	Ala	Ala	Asn	Glu	Asn	Leu	Leu	His	Gly	Ser	Gly	Leu	Ala	
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Gly	Ser	Leu	Val	Lys	Thr	Gly	Gly	Phe	Glu	Ile	Gln	Glu	Glu	Ser	Lys	
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Phe	Ala	Ile	Arg	Asn	Ile	Leu	Asp	Tyr	Val	Thr	Lys	Tyr	Asp	Leu	Arg	
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Ile	Lys	Thr	Val	Ala	Ile	Pro	Ala	Leu	Ser	Ser	Gly	Ile	Phe	Gln	Phe	
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Ser	Thr	Asp	Tyr	Gln	Glu	Val	Trp	Val	Thr	Lys	Gly	Phe	Lys	Leu	Ser	
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Cys	Gln	Tyr	Val	Phe	His	Val	Ala	Trp	His	Ser	Gln	Ile	Asn	Lys	Tyr	
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- 20 -

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 Pro Asp Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met
 385 390 395 400
 Asp Leu Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe
 405 410 415
 Ala Phe Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val
 420 425 430
 Ile Phe Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met
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 Thr Lys Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu
 450 455 460
 Ala Leu Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala
 465 470 475 480
 Gly Ser Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys
 485 490 495
 Glu Ala Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His
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 515 520 525
 Val Leu Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr
 530 535 540
 Val Ser Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp
 545 550 555 560
 Leu Ile Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln
 565 570 575
 Glu Glu Val Ala Gly Lys Arg Glu Lys Asn Leu Trp Ser Leu Ser Gly
 580 585 590
 Gln Gly Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr
 595 600 605
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 610 615 620
 Lys Lys Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln
 625 630 635 640
 Ile Asp Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met
 645 650 655
 Met Glu Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln
 660 665 670

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Gln Val Pro His Gln Phe Cys Asn Thr Val Cys Arg Val Gly Phe His
675 680 685

Arg Met Tyr Ser Thr Ser Tyr Asn Pro Val Tyr Gly Ala Gly Ile Tyr
690 695 700

Phe Thr Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser
705 710 715 720

Ser Thr Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly
725 730 735

Ser Phe Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser
740 745 750

Pro Gly Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser
755 760 765

Pro Glu Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr
770 775 780

Leu Trp Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp
785 790 795 800

Ser Gln Asp Tyr Ser Ser Gly Pro Gly Met Val Ser Ser Leu Gln Ser
805 810 815

Trp Glu Trp Val Leu Asn Gly Ser Ser Val
820 825

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<211> 2478

<212> DNA

<213> Murinae gen. sp.

<220>

<221> CDS

<222> (1)..(2478)

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ctt gaa gaa cat tat aga tgg caa att ccc att aaa cac aat gtc ttc	96
Leu Glu Glu His Tyr Arg Trp Gln Ile Pro Ile Lys His Asn Val Phe	
20 25 30	
gaa att tta aag agc aat gag agt cag cta tgt gaa gtc ctc caa aat	144
Glu Ile Leu Lys Ser Asn Glu Ser Gln Leu Cys Glu Val Leu Gln Asn	
35 40 45	
aag ttt gga tgc atc tct acc ctg agc tgt cca act cta gca ggg agc	192
Lys Phe Gly Cys Ile Ser Thr Leu Ser Cys Pro Thr Leu Ala Gly Ser	
50 55 60	

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agc tct cct gct cag aga gtc ttc aga agg acc ctg atc cct ggg ata	240
Ser Ser Pro Ala Gln Arg Val Phe Arg Arg Thr Leu Ile Pro Gly Ile	
65 70 75 80	
gag tta tct gtc tgg aag gat gac ctt acc aga cac gtt gtt gat gct	288
Glu Leu Ser Val Trp Lys Asp Asp Leu Thr Arg His Val Val Asp Ala	
85 90 95	
gtg gtg aac gca gcc aat gaa aac ctt ttg cat gga agt ggc ctg gcc	336
Val Val Asn Ala Ala Asn Glu Asn Leu Leu His Gly Ser Gly Leu Ala	
100 105 110	
gga agc ttg gtg aaa act ggt ggc ttt gaa atc caa gaa gag agc aaa	384
Gly Ser Leu Val Lys Thr Gly Gly Phe Glu Ile Gln Glu Glu Ser Lys	
115 120 125	
aga atc att gcc aac gtt ggt aaa atc tca gtt ggt gga atc gct atc	432
Arg Ile Ile Ala Asn Val Gly Lys Ile Ser Val Gly Gly Ile Ala Ile	
130 135 140	
acc ggt gcg ggg aga ctt cct tgc cat ttg att atc cat gcg gtt gga	480
Thr Gly Ala Gly Arg Leu Pro Cys His Leu Ile Ile His Ala Val Gly	
145 150 155 160	
cct cgg tgg aca gtt acg aac agc cag aca gct atc gaa tta ctg aaa	528
Pro Arg Trp Thr Val Thr Asn Ser Gln Thr Ala Ile Glu Leu Leu Lys	
165 170 175	
ttt gcc att agg aac att cta gat tat gtc acc aaa tat gat cta cgc	576
Phe Ala Ile Arg Asn Ile Leu Asp Tyr Val Thr Lys Tyr Asp Leu Arg	
180 185 190	
att aag aca gta gca att cca gcc ctg agc tct gga att ttc cag ttc	624
Ile Lys Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile Phe Gln Phe	
195 200 205	
cct ctg gat ttg tgt aca agc ata att tta gaa act atc cgg ctt tat	672
Pro Leu Asp Leu Cys Thr Ser Ile Ile Leu Glu Thr Ile Arg Leu Tyr	
210 215 220	
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Phe Gln Asp Lys Gln Met Phe Gly Asn Leu Arg Glu Ile His Leu Val	
225 230 235 240	
agc aat gag gac ccc act gtt gcg tcc ttt aaa tcc gcc tca gaa agc	768
Ser Asn Glu Asp Pro Thr Val Ala Ser Phe Lys Ser Ala Ser Glu Ser	
245 250 255	
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Ile Leu Gly Arg Asp Leu Ser Ser Trp Gly Gly Pro Glu Thr Asp Pro	
260 265 270	
gct tcc acc atg act ctt cgc atc ggc cgg ggc ctg act ctc cag att	864
Ala Ser Thr Met Thr Leu Arg Ile Gly Arg Gly Leu Thr Leu Gln Ile	
275 280 285	
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Val Gln Gly Cys Ile Glu Met Gln Thr Thr Asp Val Ile Gly Asn Ser	

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290 295 300
 gga tac atg cag gat ttt aaa tca gga cga gtg gca cag tcg att ctt 960
 Gly Tyr Met Gln Asp Phe Lys Ser Gly Arg Val Ala Gln Ser Ile Leu
 305 310 315 320

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 Arg Gln Ala Gly Val Glu Met Glu Lys Glu Leu Asp Lys Val Asn Leu
 325 330 335

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 Ser Thr Asp Tyr Gln Glu Val Trp Val Thr Lys Gly Phe Lys Leu Ser
 340 345 350

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 Cys Gln Tyr Val Phe His Val Ala Trp His Ser Gln Ile Asn Lys Tyr
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 1152
 Gln Ile Leu Lys Asp Ala Met Lys Ser Cys Leu Glu Lys Cys Leu Lys
 370 375 380

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 Pro Asp Ile Asn Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Leu Met
 385 390 395 400

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 1248
 Asp Leu Lys Lys Ser Thr Ala Ala Gln Ile Met Phe Glu Glu Val Phe
 405 410 415

 gca ttt gct aaa gag cac aag gaa aaa acg cta act gta aag att gtg
 1296
 Ala Phe Ala Lys Glu His Lys Glu Lys Thr Leu Thr Val Lys Ile Val
 420 425 430

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 1344
 Ile Phe Pro Val Asp Val Glu Thr Tyr Lys Ile Phe Tyr Ala Glu Met
 435 440 445

 aca aaa agg tcc aac gag ctg aat ctc agc ggt aat agt ggt gct tta
 1392
 Thr Lys Arg Ser Asn Glu Leu Asn Leu Ser Gly Asn Ser Gly Ala Leu
 450 455 460

 gcc ctg cag tgg tcc agt ggg gag caa aga aga ggc ggc ctt gaa gct
 1440
 Ala Leu Gln Trp Ser Ser Gly Glu Gln Arg Arg Gly Gly Leu Glu Ala
 465 470 475 480

 gga tct cct gcc atc aat ctc atg ggt gta aaa gtg gga gag atg tgt
 1488

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Gly Ser Pro Ala Ile Asn Leu Met Gly Val Lys Val Gly Glu Met Cys
 485 490 495
 gag gcc cag gaa tgg att gaa agg ttg ctg gtc tcc ctg gac cac cac
 1536
 Glu Ala Gln Glu Trp Ile Glu Arg Leu Leu Val Ser Leu Asp His His
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 1584
 Ile Ile Glu Asn Asn His Ile Leu Tyr Leu Gly Lys Lys Glu His Asp
 515 520 525
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 Val Leu Ser Glu Leu Gln Thr Ser Thr Arg Val Ser Ile Ser Glu Thr
 530 535 540
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 1680
 Val Ser Pro Arg Thr Ala Thr Leu Glu Ile Lys Gly Pro Gln Ala Asp
 545 550 555 560
 ctc att gac gca gtt atg agg att gaa tgt atg ctg tgt gac gtt cag
 1728
 Leu Ile Asp Ala Val Met Arg Ile Glu Cys Met Leu Cys Asp Val Gln
 565 570 575
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 1776
 Glu Glu Val Ala Gly Lys Arg Glu Lys Asn Leu Trp Ser Leu Ser Gly
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 Gln Gly Thr Asn Gln Gln Glu Lys Leu Asp Lys Met Glu Glu Ser Tyr
 595 600 605
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 Thr Phe Gln Arg Tyr Pro Ala Ser Leu Thr Gln Glu Leu Gln Asp Arg
 610 615 620
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 Lys Lys Gln Phe Glu Lys Cys Gly Leu Trp Val Val Gln Val Glu Gln
 625 630 635 640
 ata gac aat aag gtg ctg ctg gct gcc ttc caa gag aag aag aaa atg
 1968
 Ile Asp Asn Lys Val Leu Leu Ala Ala Phe Gln Glu Lys Lys Lys Met
 645 650 655
 atg gaa gag agg acg cca aag gga tct ggg agc caa agg ttg ttt cag
 2016
 Met Glu Glu Arg Thr Pro Lys Gly Ser Gly Ser Gln Arg Leu Phe Gln
 660 665 670
 cag gtc cca cat cag ttc tgc aat acg gtg tgc aga gtc ggc ttc cac

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2064

Gln Val Pro His Gln Phe Cys Asn Thr Val Cys Arg Val Gly Phe His
675 680 685

aga atg tat tcg aca tcc tat aac cca gtt tat gga gcc ggc ata tat
2112

Arg Met Tyr Ser Thr Ser Tyr Asn Pro Val Tyr Gly Ala Gly Ile Tyr
690 695 700

ttc acc aag agc ctc aaa aat cta gca gac aag gtc aag aaa acc tca
2160

Phe Thr Lys Ser Leu Lys Asn Leu Ala Asp Lys Val Lys Lys Thr Ser
705 710 715 720

agc aca gac aag cta atc tat gtg ttt gag gca gaa gta ctc aca ggg
2208

Ser Thr Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly
725 730 735

tcc ttc tgt cag ggt aat tcc tca aat atc atc cct cca cca ttg agt
2256

Ser Phe Cys Gln Gly Asn Ser Ser Asn Ile Ile Pro Pro Pro Leu Ser
740 745 750

cct ggg gcc tta gat gtc aat gac agc gta gtt gac aat gtt tcc agc
2304

Pro Gly Ala Leu Asp Val Asn Asp Ser Val Val Asp Asn Val Ser Ser
755 760 765

cct gaa acc att gtt gtt ttt aat ggc atg cag gcc atg ccc ctg tac
2352

Pro Glu Thr Ile Val Val Phe Asn Gly Met Gln Ala Met Pro Leu Tyr
770 775 780

ttg tgg act tgc aca cag gat agg aca ttc tca cag cat ccg atg tgg
2400

Leu Trp Thr Cys Thr Gln Asp Arg Thr Phe Ser Gln His Pro Met Trp
785 790 795 800

tca cag gac tac tca tca gga cca gga atg gtc tct tcg ctg cag tcc
2448

Ser Gln Asp Tyr Ser Ser Gly Pro Gly Met Val Ser Ser Leu Gln Ser
805 810 815

tgg gaa tgg gtc tta aat ggc agc tct gtt
2478

Trp Glu Trp Val Leu Asn Gly Ser Ser Val
820 825